

IN THE SPECIFICATION

The following are replacement paragraphs.

Page 11.

Table 1. Consolidated Human p185 HER-2 predicted B cell epitopes listed in the order of ranking by amino acid residue numbers. Asparagine (N)-linked glycosylation sites are underlined in bold.

Predictive Ranking	Residue	Amino Acid Sequence	Secondary Structure
7	27 – 45	Tgtdmklrlpaspethldm (SEQ ID NO. 1)	25 – 28 β turn; 29 – 32 α helix; 35 – 38 β turn
8 (DW5)	115 – 136	AVLDNGDPLN <u>NT</u> TPVTGASPGG (SEQ ID NO. 2)	116 – 135 β turn
9	168 – 189	LWKDIFHKNNQLALTLIDT <u>NRS</u> (SEQ ID NO. 3)	173 – 176 β turn; 177 – 181 α helix
1	182 – 216	TLIDT <u>NRS</u> RACHPCSPMCKGSRGW ESSEDCQSLT (SEQ ID NO. 4)	184 – 212 β turn/loop
6	270 – 290	ALVTYNTDTFESMPNPEGRYT (SEQ ID NO. 5)	273 – 286 β turn; 278 – 280 α helix
3	316 – 339	PLHNQEVTAEDGTQRAEKCSKPCA (SEQ ID NO. 6)	319 – 324 α helix; 324 – 336 β turn.
10 (DW1)	376 – 395	PESFDGDPASNTAPLQPE (SEQ ID NO. 7)	379 – 388 β turn
12 (DW6)	410-429	LYISAWPDSLPLDSVFQNLQ (SEQ ID NO. 8)	413-421 β turn
2	485 – 503	LFRNPHQALLHTANRPEDE (SEQ ID NO. 9)	497 – 500 β turn; 499 – 504 α helix
11	560 – 593	CLPCHPECQPQ <u>NGSV</u> TCFGPEADQCVACAH YKDP (SEQ ID NO. 10)	561 – 572 & 589 – 593 β turn; 579 – 581 α helix
4	605– 622	KPDLSYMPIWKFPDEEGA (SEQ ID NO. 11)	616 – 620 α helix
5	628 – 650	IN <u>G</u> THSCVDLDDKGCPAEQRASP (SEQ ID NO. 46)	635 – 642 β turn; 643 – 646 α helix

Table 2

HLA-A3: 167-175 (ILWKDIFHK) (SEQ ID NO. 21); 714-722 (ILKETELRK) (SEQ ID NO. 22);
754-762 (VLRENTSPK) (SEQ ID NO. 23)

HLA-B7: 1159-1167 (AARPAGATL) (SEQ ID NO. 24); 35-43 (LPASPETHL) (SEQ ID NO. 25);
1101 (LPTHDPSP) (SEQ ID NO. 26);

HLA-B27: 7-15 (CRWGLLLAL) (SEQ ID NO. 27); 897-905 (RRFTHQSDV) (SEQ ID NO. 28);
433-441 (GRILHNGAY) (SEQ ID NO. 29);

H-2K^d: 63-71 (TYLPTNASL) (SEQ ID NO. 30); 553-561 (EYVNARHCL) (SEQ ID NO. 31);
440-448 (AYSLTLQGL) (SEQ ID NO. 32);

HLA-A2: 5-13 (ALCRWGLLL) (SEQ ID NO. 33); 48-57 (HLYQGCQV) (SEQ ID NO. 34); 141-
149 (QLRSLTEIL) (SEQ ID NO. 35); 435-443 (ILHNGAYSL) (SEQ ID NO. 36); 661-
669 (ILLVVVLGV) (SEQ ID NO. 37); 789-797 (DLTSTVQLV) (SEQ ID NO. 38); 851-
859 (VLVKSPNHV) (SEQ ID NO. 39); 369-378 (KIFGSLAFL) (SEQ ID NO. 40); 654-
663 (IISAVVGIL) (SEQ ID NO. 41);

Table 4. HER-2 B-cell epitope chimeric constructs incorporating promiscuous helper T cell epitope from tetanus toxoid (TT 580-599) at the C-terminus and a GPSL linker joining the two epitopes. Also shown is the % homology of the HER-2 B-cell epitope sequences with corresponding sequences in rat NEU. Note: Cys 331 -> Ala 331 change in the construct HER-2 (316-339) TT is underlined.

Chimeric HER-2 B-Cell Epitope Constructs	% Homology with rat NEU
HER-2 (27-45)-TT: NH ₂ TGTDMLRLPASPETHLDM- <u>GPSL</u> - NSVDDALINSTIYSYFPSV-COOH (SEQ ID NO. 43)	100
HER-2 (316-339) TT: NH ₂ PLHNQEVTAEDGTQRAEKCSKPCA- <u>GPSL</u> -NSVDDALINSTIYSYFPSV-COOH (SEQ ID NO. 44)	88.5
HER-2 (485-503)-TT: NH ₂ LFRNPHQALLHTANRPEDE- <u>GPSL</u> - NSVDDALINSTIYSYFPSV-COOH (SEQ ID NO. 45)	80